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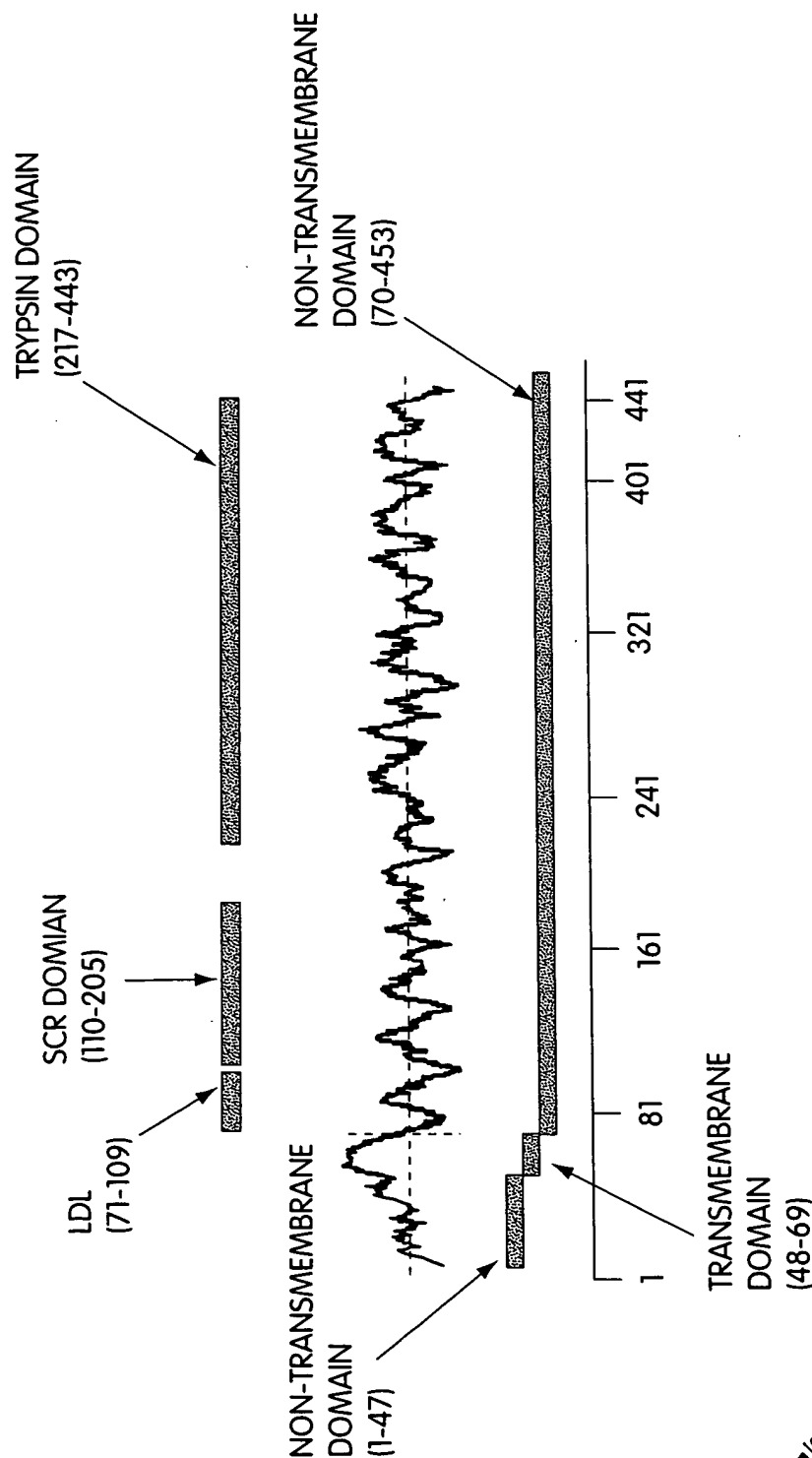
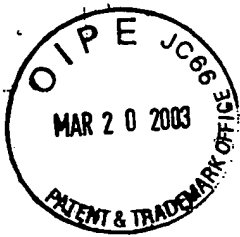


Fig. 1

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trypsin: domain 1 of 1, from 217 to 443: score 293.0, E = 3.2e-92  
\*->IvGGreaqpgsfsgPwqvsIqvrsgggsrkhfCGGSLisenwVLTAA  
IvGG + ++ Pwq+slq+ + +h+CGGS+i + w++TAA  
14094 217 IVGGNMSLLSQW--PWQASLQFQG-----YHLCGGSVITPLWIITAA 256  
  
HCvsgaasapassvrVslsvrlGehnlsltegteqkfdvkktiivHpnyn  
HCv++ +++s+++ +G +sl + v+k i+ H++y  
14094 257 HCVYD--LYLPKSWTI----QVGL--VSLLDNPAPSHLVEK-IVYHISKYK 297  
  
pdtldngaYdnDiAlLkLkspgvtlgdtrpicLpsassdlpvGttctvs  
p+ l+ nDiAl+kL++p +t+++ ++p+cLp + ++p+G c+ s  
14094 298 PKRLG-----NDIALMKLAGP-LTFNEMIQPVCLPNSEENFPDGKVCWTS 341  
  
GwGrrptknlgl.sdtLqevvvpvvsretCrsayeyggtDkvefvtdnm  
GwG t+++g+ s +L ++ vp++s++ C+++ ygg +++ m  
14094 342 GWGA--TEDGGdASPVLNHAAPLISNKICNHRDVYGGI-----ISPSM 383  
  
iCagal.ggkdaCqGDSGGPLvcsgnrdgrwelvGivSwGsygCargnk  
+Cag+l+gg+d+CqGDSGGPLvc w+lvG +S+G gCa+ nk  
14094 384 LCAGYLTGGVDSCQGDGGPLVCQER---RLWKLVGATSFG-IGCAEVNK 429  
  
PGvytrVssyldWI<-\*  
PGvytrV+s+ldWI  
14094 430 PGVYTRVTSFLDWI 443

Fig. 2A

trypsin\_2: domain 1 of 1, from 216 to 443: score 328.2, E = 9.2e-95  
\*->RIVGGseakigsfPWqvsLq.....CGGSLIsprwVLTAAHC....  
RIVGG+ + ++PWq+sLq ++ + CGGS+I+p w++TAAHC +  
14094 216 RIVGGNMSLLSQWPWQASLQfqqyhlCGGSVITPLWIITAAHCvdyd 262  
  
.....rVrLgshdlssgeeteggprldspggqvikVskiievHpnYn..  
+++ ++ +G +l + + + V+ki+ H +Y ++  
14094 263 ylpkswTIQVGLVSLLDNP-----APSHLVEKIV-YHISKYKpk 299  
  
...NDIALLkLkepvtlsdsntvrPicLPssneiktsegntvpaGttctV  
+ +NDIAL+kL+ p+t+++ ++P+cLP+s ++++p+G c+  
14094 300 rlgNDIALMKLAGPLTFNE--MIQPVCLPNS-----EENFPDGKVCWT 340  
  
sGWGrtsegpeesgggslpdlqevnvpiivsnetCr.....Ml  
sGWG t++ gg + vL ++ vp++sn+ C++++ ++ ++Ml  
14094 341 SGWGATED-----GGDASPVLNHAAPLISNKICNhrdvvggiispsML 384  
  
CAGyleggntpgGkDaCqGDSGGPLvc.....vLvGiVSWGssslgCa  
CAGyl+ gG+D+CqGDSGGPLvc++++ ++LvG +S+G +gCa  
14094 385 CAGYLT-----GGVDSCQGDGGPLVCqerrlwKLVGATSFG----IGCA 425  
  
rpnkPGVYTrVssyldWI<-\*  
+ nkPGVYTrV+s+ldWI  
14094 426 EVNKPVG YTRVTSFLDWI 443

Fig. 2B

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BEGIN SEQ ID NO: 6      END SEQ ID NO: 6

\*->stCggpdeFqCgsgrrCIprswvCDGdpDCeDGSDEslenCaa<-\*

14094    71      +C+    +++C+s+    CI    +CDG    DC+DG+DE    +C++      109

FDCS--GKYRCRSSFKCIELIARCDGVSDCKDGEDE--YRCVR

Fig. 3A

BEGIN SEQ ID NO: 7

\*->vgGssrCeGrVEVrhgskWgtVCdssWslrdanvdpQaskvCrqLG

14094    110      vgG    +++    +++V+    +    W+t    C+++W    +    anv    +C+qLG

VGG--QNA-VLQVF-TAASWKTMCSDDWKGHYANV-----ACAQLG 146

CGgavsl1.gpyfsegggPagqreiwldgvnCsGnE...tsLsqCpvrvt

14094    147      +    VS+    +    s+    g    ++++++    +    ++++    +++

FPSYVSSDnLRVSSLEG-----QFREEFVSIDHllpdDKVTALHHS-- 187

ppglrqqcshdgedagVvCs<-\*

14094    188      ++    ++C    g+    ++C      END SEQ ID NO: 7

-VYVREGCAS-GHVVTLQCT      205

Fig. 3B



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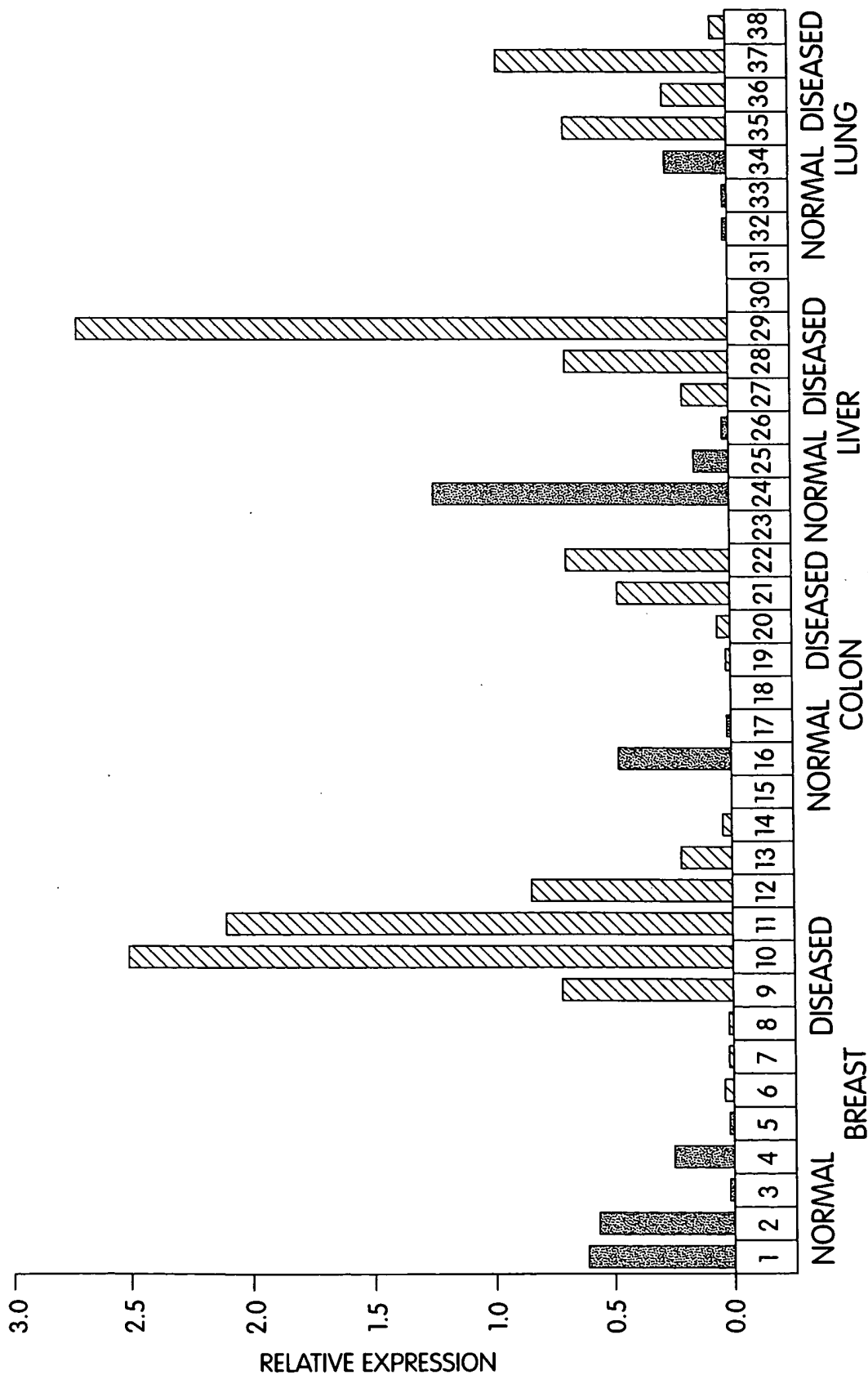


Fig. 4



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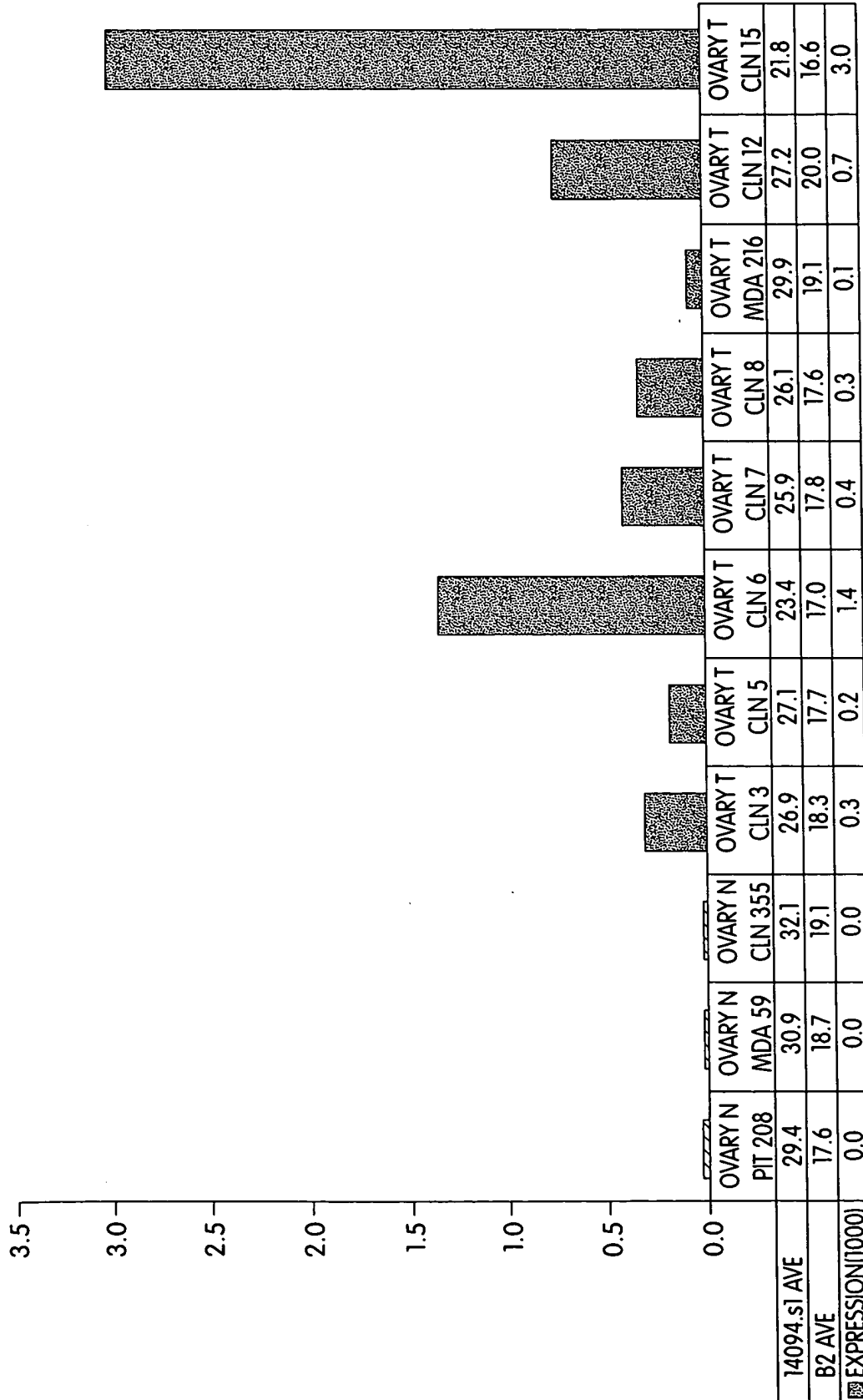


Fig. 5



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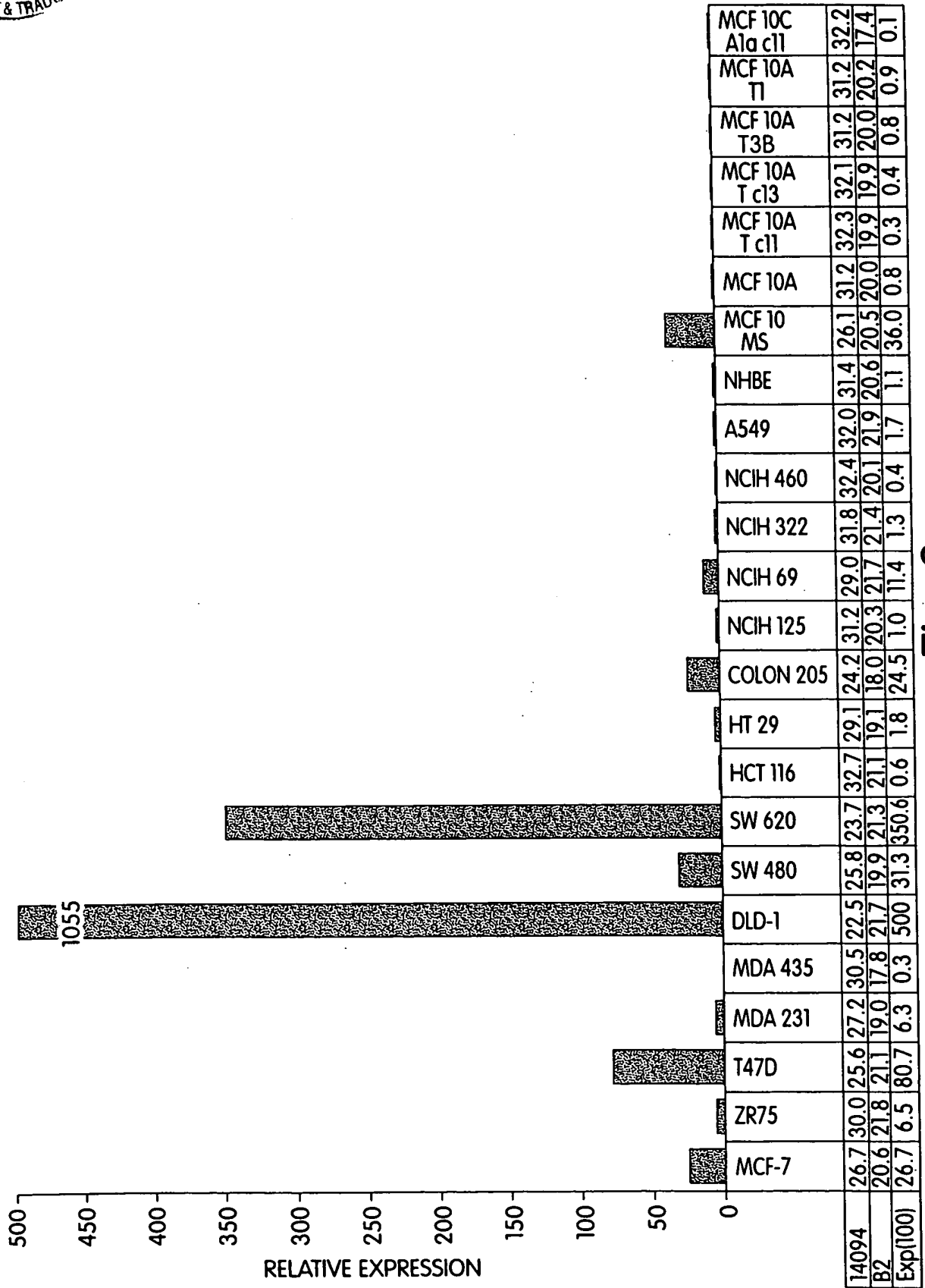


Fig. 6